marked-up version of the claims. 37 C.F.R. §1.121 (c)(l)(ii).

II. REMARKS

The July 19, 2002 Office Action notes that dependent claims 24-26, 28-31, 39 and 40 are allowable if amended to overcome any Section 112 rejections, and if amended into independent form, where necessary.

On December 17, 2002, Applicant submitted a Communication amending claims 23, 28, 29, 31, 32 and 40 for the purposes of addressing the Section 112 rejections. In a telephone conference between the Examiner and the undersigned on December 18, 2002, the Examiner indicated that the amendments overcame the Section 112 rejections.

In this Response, all claims rejected on prior art are canceled, and the allowable claims are put into independent form by incorporating the claim(s) from which they depended, as appropriate, which claims have been noted as complying with Section 112.

III. CONCLUSION

In light of the above amendments and remarks, it is respectfully submitted that claims 24-26, 28-31 and 39-40 are now in condition for allowance.

If there are any additional fees associated with this Response, please charge same to our Deposit Account No. 19-3935.

Finally, if there are any formal matters remaining after this Response, the undersigned would appreciate a telephone conference with the Examiner to attend to these matters.

Respectfully submitted,

STAAS & HALSEY LLP

Date: 12/19/02

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CERTIFICATE OF FACSIMILE TRANSMISSION

I hereby certify that this correspondence is being transmitted via facsimile to: The U.S. Patent and Trademark Office, Washington, D.C. 20231
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VERSION WITH MARKINGS TO SHOW CHANGES MADE

IN THE WRITTEN DESCRIPTION:

Please AMEND the Written Description as follows:

On page 2, first full paragraph, please amend as follows:

The DNA having the composition called a polynucleotide strand is formed by a strand of the above listed four bases, that is, the adenine A, guanine G, cytosine C, and thymine T, bound in a series. For example, if a DNA is extracted from the chromosome in the cell of a human being and is arranged as a sequence, it can be as long as 1 meter and contain[s] 3 billion bases.

On page 2, second full paragraph, please amend as follows:

Thus, a DNA has a strand of bases, that is, a base sequence linked in the form of a strand. The strand is normally very long. In genetic engineering, a DNA [comprising] including various genes is cleaved for gene recombination, and a DNA fragment having [a] specific genetic information is extracted from a number of the cleaved DNA fragments. The extracted DNA fragments, that is, object DNA fragments, should be normally proliferated.

On page 6, third full paragraph, please amend as follows:

FIG. 3 shows the vector used in the DNA cloning process and the multiple cloning site in the vector. A number of restriction enzyme sites to be cleaved by various restriction enzymes [are] is concentrated in the multiple cloning site.

On page 7, second full paragraph, please amend as follows:

Recently, [the] computer technology has been utilized as one of the sequence methods, thereby enabling an enormous volume of data to be input and accumulated. Thus, computers are required in determining the base sequence.

On page 11, second paragraph, please amend as follows:

A vector unit base sequence removing method according to the invention is used for removing a vector unit base sequence from a DNA base sequence which is obtained as a result of performing a cloning process by integrating an object DNA fragment into a vector, and

includes the vector unit base sequence as a part of a base sequence of the vector and the object DNA fragment. The method [comprises] includes the steps of: generating a retrieval base sequence as a retrieval key for use in retrieving the vector unit base sequence from the DNA base sequence based on the vector, a restriction enzyme used to cleave the vector for cloning the cloning process, and a restriction enzyme used to obtain the object DNA fragment; specifying the vector unit base sequence using the retrieval key; and removing the specified vector unit base sequence to specify the object DNA fragment.

On page 12, first paragraph, please amend as follows:

The retrieval key may [comprise] include a forward (leading) retrieval key and a backward (following) retrieval key for respectively identifying areas before and after the object DNA fragment in the DNA base sequence. The forward and backward retrieval keys may indicate the base sequences corresponding to restriction enzyme sites including parts of the vector cleaved by a restriction enzyme for the cloning process and ends of the object DNA fragment.

On page 12, last paragraph extending over to page 13, please amend as follows:

The method according to the present invention may further [comprise] include the steps of: performing homology retrieval on condition that a similarity value indicating a matching rate between the retrieval base sequence and the DNA base sequence is equal to or larger than a predetermined value in retrieval using the retrieval key for the DNA base sequence; and obtaining a candidate for a base sequence at a junction between the vector in the DNA base sequence and the object DNA fragment according to a result of the homology retrieval.

On page 13, first paragraph, please amend as follows:

The method according to the present invention may further [comprise] include the steps of: generating a second forward retrieval key by adding to the forward retrieval key a portion that should be existing before the multiple cloning site of the vector; performing a second homology retrieval on condition that a second similarity value indicating a matching rate between a base sequence corresponding to the second forward retrieval key and a base sequence including a base sequence at a junction of the DNA base sequence is equal to or larger than a predetermined value; and obtaining as a vector unit candidate for the vector unit base sequence an area specified as a result of the second homology retrieval and an area or

areas before the specified area.

On page 13, last paragraph extending over to page 14, please amend as follows:

The method according to the present invention may further [comprise] include the steps of: generating a second backward retrieval key by adding to the backward retrieval key a portion that should be existing after the multiple cloning site of the vector; performing a second homology retrieval on condition that a second similarity value indicating a matching rate between a base sequence corresponding to the second backward retrieval key and a base sequence containing the base sequence at the junction of the DNA base sequence is equal to or larger than a predetermined value; and obtaining as a vector unit candidate for the vector unit base sequence an area specified as a result of the second homology retrieval and an area or areas after the specified area.

On page 14, last paragraph extending over to page 15, please amend as follows:

The method according to the present invention may further [comprise] include the steps of: generating a second forward retrieval key by adding to the forward retrieval key a portion that should be existing before the multiple cloning site of the vector; generating a second backward retrieval key by adding to the backward retrieval key a portion that should be existing after the multiple cloning site of the vector; performing a second homology retrieval on condition that a second similarity value indicating a matching rate between a base sequence corresponding to the second forward retrieval key and a base sequence including a base sequence at a junction of the DNA base sequence is equal to or larger than a predetermined value, and a third similarity value indicating a matching rate between a base sequence corresponding to the second backward retrieval key and a base sequence including the base sequence at a junction of the DNA base sequence is equal to or larger than a predetermined value; obtaining as a forward vector unit candidate for the vector unit base sequence a forward area specified as a result of the second homology retrieval and an area before the forward area; and obtaining as a backward vector unit candidate for the vector unit base sequence a backward area specified as a result of the second homology retrieval and an area after the backward area.

On page 15, last paragraph extending over to page 16, please amend as follows:

A vector unit base sequence removing device according to the invention is for removing

a vector unit base sequence from a DNA base sequence which is obtained as a result of performing a cloning process by integrating an object DNA fragment into a vector and includes the vector unit base sequence as a part of a base sequence of the vector and the object DNA fragment. The device [comprises] includes: a first unit for generating a base sequence as a retrieval key for use in retrieving the vector unit base sequence from the DNA base sequence based on the vector, a first restriction enzyme used to cleave the vector for the cloning process, and a second restriction enzyme used to obtain the object DNA fragment; a second unit for specifying the vector unit base sequence using the retrieval key; and a third unit for removing the specified vector unit base sequence to specify the object DNA fragment.

On page 16, first full paragraph, please amend as follows:

The device according to the present invention may further [comprise] include: a vector list storage unit for storing a vector list; and a restriction enzyme list storage unit for storing a restriction enzyme list. The vector is specified in the vector list, and the first and second restriction enzymes are specified in the restriction enzyme list.

On page 16, second full paragraph, please amend as follows:

The device according to the present invention may further [comprise] include a display unit. The vector may be specified in the vector list displayed on the display unit, and at least one of the first and second restriction enzymes may be specified in the restriction enzyme list displayed on the display unit.

On page 16, last paragraph extending over the page 17, please amend as follows:

The device according to the present invention may further [comprise] include a program storage unit for storing at least one of: a program for generating the retrieval key by controlling the first unit; a program for specifying the vector unit base sequence by controlling the second unit; and a program for removing the vector unit base sequence by controlling the third unit.

On page 21, after the seventh paragraph, please amend the heading as follows:

Description of the Preferred Embodiments

On page 21, last paragraph extending over to page 22, please amend as follows:

FIG. 5 is a block diagram showing the functions of an automatic vector unit removing

method of the automatic vector unit removing method of the present invention. In [genetics] general, the vector, for example, a circular plasmid DNA molecule, is cleaved, and an object DNA fragment is integrated into the cleaved portion in a cloning process. The automatic vector unit removing method according to the present invention removes the base sequence of a portion of the vector unit contained in the object DNA fragment from the object DNA fragment retrieved from the vectors generated [in] through the DNA cloning process.

On page 25, first full paragraph, please amend as follows:

FIG. 6 is a flowchart showing the basic process of the automatic vector unit removing method according to the present invention. As shown in FIG. 6, the method [comprises] includes steps S6 through S9. In step S6, the type of the vector used in the cloning process is selected from the vector list and entered. In step S7, the restriction enzyme used in the cloning process is selected from the restriction enzyme list and entered. In step S8, a retrieval key is generated based on the information about the vector and restriction enzyme, and the vector unit is retrieved according to the retrieval key. That is, the homology between the retrieval key and the multiple cloning site is checked, and the vector unit specification program is executed to select the vector unit. In step S9, the vector unit specified by the vector unit specification program is removed, thus terminating the process.

On page 28, last paragraph, extending over to page 29, please amend as follows:

After the used vector [are] is selected and the multiple cloning site and the restriction enzyme information are extracted in step S13 in FIG. 7, in steps S14 through S17, four restriction enzymes used in cleaving the DNA strands at the 5' and 3' are selected according to extracted information. The selection is made by specifying used restriction enzymes from the restriction enzyme list shown in FIG. 11. FIG. 11 shows a list of the restriction enzymes used when PUC 18 is selected as a vector. The restriction enzyme list stores the restriction enzymes for use in cleaving the restriction enzyme site in the multiple cloning site of the vectors.

On page 29, second full paragraph, please amend as follows:

FIG. 12 is a flowchart showing the vector unit [specificating] specification and deleting program in step S18 shown in FIG. 7. This process [comprises] includes steps S21 through S25.

On page 36, first full paragraph, please amend as follows:

If it is determined in step S31 that the single-stranded area on the object DNA fragment 5' side is not located on the 5' side (no in S31), and if it is determined in step S32 that the base sequences of the single-stranded area do not match each other even if the single-stranded area [is] exists (no in S32), then it is determined in step S34 that the restriction enzyme has been mistakenly selected, and control is returned to the restriction enzyme selecting process, thereby repeating the process.

On page 38, first full paragraph, please amend as follows:

FIG. 16 is a flowchart showing the process of determining the retrieval key on the 3' side. Since the flowchart is almost the same as that for the 5' side as shown in FIG. 15, the detailed explanation is omitted here. Steps S40 through S49 shown in FIG. 16 correspond to steps S30 through S39 in FIG. 15. If the single-stranded areas of the restriction enzyme sites to be located on the vector 3' side and object DNA fragment 3' side are actually located on the 5' side, then [F2A] + [F2B5] + [V2C] is defined as the retrieval key on the 3' side. If the single-stranded areas on the 3' side do not exist, then [F2A] + [V2C[{]] is defined as the retrieval key on the 3' side. If the single-stranded areas exist on the 3' side, then [F2A] + [V2B3] + [V2C] is defined as the retrieval key on the 3' side.

On page 39, last paragraph extending over to page 40, please amend as follows:

FIG. 18 is a flowchart showing the process of retrieving the primary candidate for the boundary on the 5' side using the 5' side retrieval key shown in FIG. 17. When the process starts as shown in FIG. 18, the homology retrieval is performed in the base sequence of the object clone using the 5' side retrieval key in step S51. The retrieval keys and [a] retrieval results obtained as areas indicating a homology exceeding a predetermined value (the number of bases matching in, for example, 6 bases) are listed as primary candidates for boundary portions in step S52, then terminating the process.

On page 45, second full paragraph, please amend as follows:

The methods and processes described above can be realized using an automatic control device such as a computer. As shown in Fig. 25, the control device according to the invention [comprises] <u>includes</u> a processing device 10, memory 20, display 30, input unit 40,